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FIG. 1

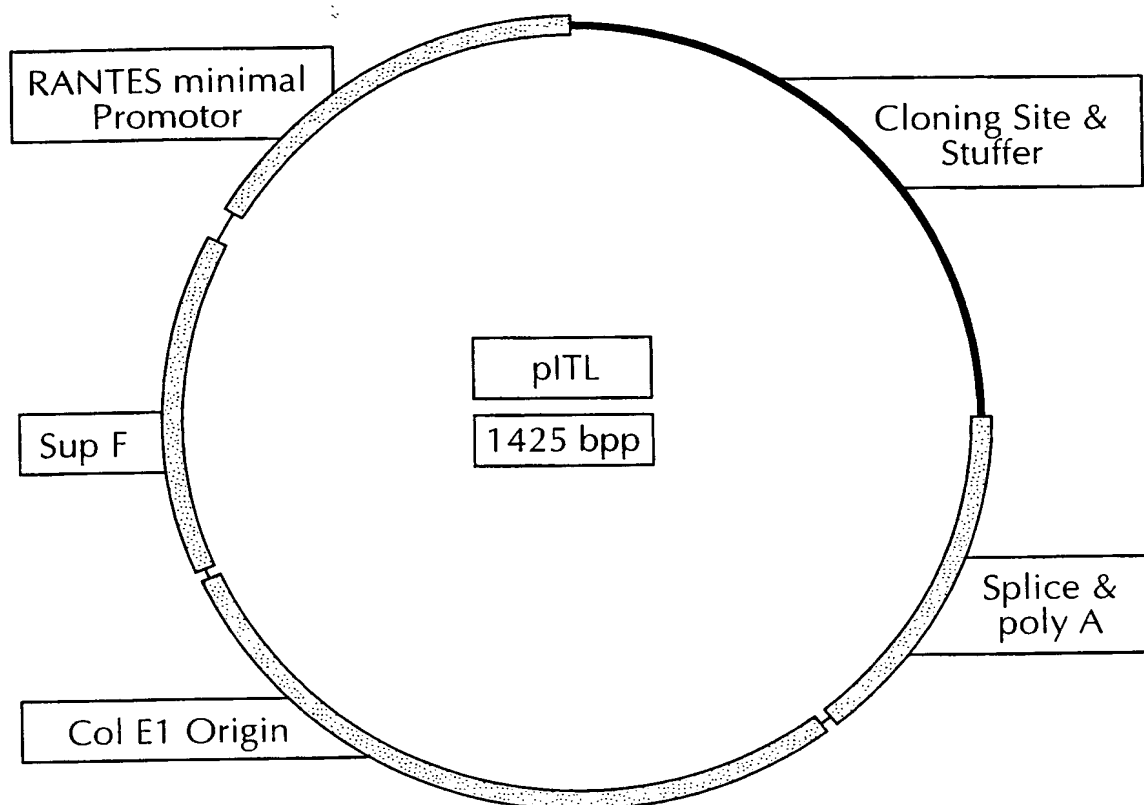
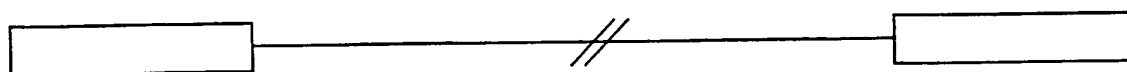


FIG. 2



GCCA/CCATGGC
CGGTGGT/ACCG

GCCT/TAAGGCG
CGGAATT/CCCG

FIG. 3A

MRPSGTAGAAALLAALCPASRALEEKKVCQGT	60	SNKLTQLGTFEDHFLSLQRMFNCEVVLGNLEITYVQRNYD
M---	57	ELAAALCRWGLLLALLP-PGA-AST-VCTGTDMLRLPASPETHLDMLRHL
		YQGCQVVOGNLELTYLPTNAS
LSFLKTIQEVAGYVLI	125	ALNTVERIPLENLQIIRGNMYENS
		YALAVLSNYD--AN---KT----
		GLKELPMRNL
LSFLQDIOEVQGYVLI	140	AHNQVRQVPLQRLRIVRG
		QTLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSL
		147
		122
QEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDFQNH	175	LGSCQKCDPSCNGS-CWGAGEENCQKLT
		KIIL
TEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQALTLIDTNR	175	SRACHPCSPMCK-GSRCWGESSEDCQSL
		TRTV
		289
CAQOCSGRCRGKSPSDCCHNQCAAGCTGPRESDCLVCRKFRDEAT		CKDTCPPMLYNPTTYQMDVNP
		EGKYSFGA
CAGGCA-RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLFHNSG		ICELHCPALVTYNTDTFESMPNP
		EGRYTFFGA
		295
		350
		*
YVVTDHGSCVRACGADSYEME-EDGVRKCKKCEGPCRKVCN		GIGIGEFKDSLSINATNIKFNCT
		SISGDLHIL
YLSTDVGSC		TLVCP
		LNQEVTAEDGTQRCCKSPCARVCYGLGMEHLREVR
		AVTSANIQEFAGCKKIFGSLAFL
		352
		438
PVAFRGDSFTHTPPLDPQELDILKTVKEITGFLLIQAWPENRTDL		HAFENLEIIRGRTKQPGQFSLAVVSLNITS
		PESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSL
		PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISW
		445

[illegible]

FIG. 3B

LGLRSLKEISDGDVIIISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSCKATGQVCHALCSPEGCGWGPEPRD
|||||: | : ||||: | : ||||: | : ||||: | : ||||: | : ||||
LGLRSLRELGSLALIHHNTHLCFVHTVPWDQLFRNP HQALL HTANRPED ECVGE GLACH Q LCARGHC WGPGPTQ

475 * *

500

CVSCRNVSRGRECVDKLLLEGEPREFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPA
CVNCSQFLRGQECVEECRVLQGLPREYVYNARHCLPCHPECPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPS

GVMGENTLV-WKYADAGHVCHLCHPNCTYCGTGPGLEGCP TNGPKIPSIATGMVGALLLLVVAL---GIGLF
631 * * *
GKVPDL SYMPIWKFPDEEGACQPCPINCTHSCVDLDKGC PAEQRASPLTSII SAVVGILLVVVLGVVFGI-LI
644

[illegible]

775
VAIKELREATSPKANKEILDEAYVMA SVDNPHVCRLLGICLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLN
VAIKVLRENTSPKANKEILDEAYVMA GVSYPVSRLLGICLTSTVQLVTQLMPYGCLLDHVTENRGRLGSDLLN

WCVQIAKGMNyleDRRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMALESILHRIY
||| ||| ||| ||| ||| ||| : ||| ||| ||| ||| ||| :
WCMQIAKGMSyleDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRF

850 850 892

FIG. 3C

929

THQSDVWSYGVTWELMTFGSKPYDGI PASEISSILEKGERLPQPPICTIDVYMIMVKCWMIDADSRPKFRELII
:
THOSDVWSYGVTWELMTFGAKPYDGI PAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVS

940

[illegible]

1000

```

--SSPSTSRTPLLSSLATSNNSTVACIDRN--GLQSCPIKEDSFLQRYSSDPTGAL-T
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
RSSSTRSGGDLTLGLEPSEEEAPRSLAPSEGAGSDVFDGDLGMAAKGLQSLPTHDPSPLORYSEDPTVPLPS

```

[illegible]

1120

1150
TFDSTFLPVPEYINQ-SVPKRPAGSVQNVPVYHNQLNPAPSRDPHYQDPHSTA VGNPEYLNTVQPTCVNSTFDSP
| | | | : | | : | | :
TPQGTCSPQPEYVNQPDVRPQPSPREGPLPAARPAGATLERPKTLSPGKNGVKDVFAFGGA VENPEYLTPQGG
1300

1300

AHWAQKGSHQ-ISL--DNPDYQ-QDFFPKEAKPNGIFKGST--AENAEYL-R-VAPQSSEFIGA
AAP-QPHPPPAFSPAFDNLYYWDQDPPPERGAPPS-TFKG-TPTAENPEYLGLDVPV

1255

FIG. 4A

57
MELAAALCRWGLLLALLPPGAASTQVCTGTMKLRLLPASPETHLDMRLHLYQGCQVQGNLELTYPNTNASLS
60
MIIMELAAWCRWGFLALLPPGIAGTQVCTGTMKLRLLPASPETHLDMRLHLYQGCQVQGNLELTYPVPANASLS

117
FLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTOQLFEDNYALAVLDNGDPLNNTTPVT-GASPGGLRELQRLSLT
120
FLQDIQEVQGYMLIAHNQVKRVPLOQLRIRIVRGTOQLFEDKYALAVLDNRDPQDNVAASTPGRTP EGLRELQRLSLT

176
EILKGGVLIQRNPQLCYQDTILWKDIFHKNNQALTLIDTNRSRACHPCSPMCKGSRWCGESSEDCQSLTRTVCA
180
EILKGGVLIQRNPQLCYQDMVLWKDVFRKNNQAPVDIDTNRSRACPPCAPACKDNHCWGESPEDCQILGTICT

236
GGCARCKGRLPTDCCHEQCAAGCTGPKHSDCLACLFHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCV
240
SGCARCKGRLPTDCCHEQCAAGCTGPKHSDCLACLFHFNHSGICELHCPALVTYNTDTFESMHNPEGRYTFGASCV
296
300

356
TACPYNLSTDVGSCTLVCPLHNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIF
360
TTCYPYNLSTEVGSCTLVCPPNNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLRGARAITSDNVQEFDFGCKKIF

416
GSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPLDSVFQNLQVIRGRILHNGAYSLTLQ
420
GSLAFLPESFDGDPSSGIAPLRPEQLQVFETLEEITGYLYISAWPDSLRLDSVFQNLRIIRGRILHHDGAYSLTLQ

65 T 0 1 1 " 2 0 2 4 2 5 0

FIG. 4B

476
GLGISWLGLRSLRELGSLGLALIHNNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDE-CVGEGLACHQLCARGHC
|||||
GLGIHSLGLRSLRELGSLGLALIHNAHLCFVHTVPWDQLFRNPHQALLHSGNRPEEDLCVSSGLVCNSLCAHGHC
480
535
WGPGETQCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPONGSVTCFGPEADQCVACAHYKDPFF
595
WGPGETQCVNCSHFLLRGQECVEECRVWKGLPREYVSDKRCLPCHPECQPONSSETCFGSEADQCAACAHYKDSSS
600
540
655
CVARCPGSKPDLSYMPIWKFPDDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIIISAVVGILLVVVLGVV
660
CVARCPGSKPDLSYMPIWKYPDEEGICQPCPINCTHSCVDLDERGCPAEQRASPVTFIIATVEGVLFLFLVVV
710
715
EGILI_KRR-QQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPD
770
775
GENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPIVSRLLGICLTSTVQLVTQIMPYGCLLDHVRENRRL
830
835
GSQDLNWCMIQAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEHADGGKVPKWMMALE
870
896
GSQDLNWCMIQAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEHADGGKVPKWMMALE

FIG. 4C

SILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGI
PAREIPDLLEKGERLPQPPICTIDVYMIMVKWMIDSECRP
SILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGI
PAREIPDLLEKGERLPQPPICTIDVYMIMVKWMIDSECRP
950
955

RFRELVSEFSRMARDPQRFVVIQNE
DLGPASPLDSTFYRSLLEDDDDMGDLVDAE
EYLVPOQGFFCPDPAPGAGGM
RFRELVSEFSRMARDPQRFVVIQNE
DLGPSSPMDSTFYRSLLEDDDDMGDLVDAE
EYLVPOQGFFSPDPTPGTGST
1010
1015

VHHRSSSTRSGGDLTLGLEPSEEEA
PRSLAPSEGAGSDVFDGDLGMGA
KGLQSLPTHDPSPLOQYSEDPT
AHRHRSSSTRSGGDLTLGLEPSEEE
GPPRSLAPSEGAGSDVFDGDLAMGV
TKGLQSLSPHDLSPLOQYSEDPT
1070
1075

VPLPSETDGYVAPLTCSPQPEYVNQ
PDVVRPQPPSPREGPLPAARPA
GATLERPKTLSPGKNGVVKDVFAFGGAVE
LPLPETDGYVAPLACSPQPEYVNQ
SEVQPQPLTPEGPLPPVRPA
GATLERPKTLSPGKNGVVKDVFAFGGAVE
1130
1135
1193
1198

NPEYLTPOQGAAPQHPHPPAFSPA
FDNLYYWDQDPPERGAPSTFKGT
PTAENPEYLGLDVPV
NPEYLVPREGTASPPHPPAFSPA
FDNLYYWDQNSSEQPPPSNFEGT
PTAENPEYLGLDVPV
1255
1263

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FIG. 5

